

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 23, 2003, 15:20:58 ; Search time 2393 Seconds
(without alignments)
15773.026 Million cell updates/sec

Title: US-09-745-506-74

Perfect score: 1553
Sequence: 1 GTGATTCGTTATCTTGTCCT.....TCGTCTTACTTAACATTCAA 1553

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size : 0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST: *
1: em_estbda: *
2: em_esthum: *
3: em_estlin: *
4: em_estnu: *
5: em_estrov: *
6: em_estrpl: *
7: em_estro: *
8: em_hlc: *
9: gb_est1: *
10: gb_est2: *
11: gb_hlc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: em_gss_hum: *
18: em_gss_inv: *
19: em_gss_pln: *
20: em_gss_vit: *
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22: em_gss_man: *
23: em_gss_mus: *
24: em_gss_pro: *
25: em_gss_rtd: *
26: em_gss_phg: *
27: em_gss_vrl: *
28: gb_gss1: *
29: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	ID	Description
1	858	55.2	930	13 BX393871	BX393871 BX393871
2	833	53.6	857	13 B0172435	B0172435 AGENCOURT
3	827	53.3	1201	9 AL581997	AL581997 AL581997
4	808	52.0	1201	13 BX446370	BX446370 BX446370

5	787	50.7	957	9 AL521920	AL521920 AL521920
6	784	50.5	1117	12 BM545164	BM545164 AGENCOURT
7	769	49.5	836	13 B0229243	B0229243 AGENCOURT
8	763	49.1	1201	9 AL529615	AL529615 AL529615
9	732	47.1	1019	13 B0859307	B0859307 AGENCOURT
10	722	46.5	1019	12 BM557530	BM557530 AGENCOURT
11	720	46.4	890	9 AL520538	AL520538 AL520538
12	677	43.6	759	12 BE275324	BE275324 601122173
13	675	43.5	919	13 B0526538	B0526538 AGENCOURT
14	674	43.4	877	13 B0437698	B0437698 AGENCOURT
15	652	42.0	963	10 BE797115	BE797115 601587094
16	646	41.6	909	14 CD385139	CD385139 AGENCOURT
17	640	41.2	728	14 CD102399	CD102399 AGENCOURT
18	627	40.4	762	12 BG676203	BG676203 602718981
19	626	40.3	1031	13 BX385102	BX385102 BX385102
20	622	40.1	742	12 B1093955	B1093955 602857854
21	611	39.3	817	12 B1755123	B1755123 603022837
22	609	39.2	859	10 BF975933	BF975933 602246134
23	609	39.0	888	13 B0195469	B0195469 AGENCOURT
24	605	38.5	945	10 BE747311	BE747311 601580280
25	598	38.5	909	13 B0165031	B0165031 AGENCOURT
26	594	38.2	958	10 BF973889	BF973889 602242014
27	593	38.2	845	10 BG754550	BG754550 602710167
28	592	38.1	985	13 BQ927763	BQ927763 AGENCOURT
29	590	38.0	843	13 B0848893	B0848893 AGENCOURT
30	590	38.0	1074	13 BX339176	BX339176 BX339176
31	581	37.4	980	13 B0854847	B0854847 AGENCOURT
32	574	37.0	666	13 B0663511	B0663511 C1102C03
33	569	36.6	807	12 B1766329	B1766329 603052429
34	568	36.6	568	14 CB122465	CB122465 K-EST0170
35	568	36.5	732	10 BG472953	BG472953 602514888
36	567	36.5	796	9 AU134237	AU134237 AU134237
37	566	36.4	638	14 CB122989	CB122989 K-EST0171
38	563	36.3	1119	10 BG745052	BG745052 602723147
39	559	36.0	610	12 BM841141	BM841141 K-EST0118
40	557	35.9	600	14 CB146277	CB146277 K-EST0201
41	555	35.7	1201	9 AL523986	AL523986 AL523986
42	549	35.4	549	12 BM712181	BM712181 UI-E-DW1-
43	549	35.4	871	12 BG765986	BG765986 602738046
44	549	35.4	921	10 BG335331	BG335331 602404158
45	546	35.2	753	10 AM957667	AM957667 EST369737

ALIGNMENTS

RESULT 1 BX393871 930 bp mRNA linear EST 13-MAY-2003
LOCUS BX393871 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
DEFINITION CDNA clone CS0DC005YM21 5-PRIME, mRNA sequence.

ACCESSION BX393871.1 GI:30624084
VERSION
KEYWORDS
SOURCE

ORGANISM Homo sapiens (human)
EST.

REFERENCE 1 (bases 1 to 930)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length CDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1287.f for
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=CS0DC005AG101p1cluster-1287.f. Contact :
Feng liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600

FEATURES Faraday Avenue Genoscope sequence ID : CS0DC005AG110P1.
Location/Qualifiers
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source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC005YM21"
/issue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 248 a 231 c 214 g 237 t

Query Match 55.2%; Score 858; DB 13; Length 930;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 858; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

188 GTCCCGACGACGATCGGTTGTAGATTCCTGATTCGCAATTCCTCCGTTCTTCATG 247
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73 GTCCCGACGACGATCGGTTGTAGATTCCTGATTCGCAATTCCTCCGTTCTTCATG 132
|||||
248 GATTGAAGGCTCTCTTCTTCTTCTTGAATGACTTTCATCCCTCTGTTGCTGAGAGT 307
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133 GATTGAAGGCTCTCTTCTTCTTCTTGAATGACTTTCATCCCTCTGTTGCTGAGAGT 192
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308 TGGGACATGTTGGATTACTGGTGAACCAAGCCACACATCTGTAATATACATCTTC 367
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193 TGGGACATGTTGGATTACTGGTGAACCAAGCCACACATCTGTAATATACATCTTC 252
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368 CTGACCAATGACCTGACTGAGAAAGATGAGAGAGTGTCTGCAAAAAGAGGACACCTC 427
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253 CTGACCAATGACCTGACTGAGAAAGATGAGAGAGTGTCTGCAAAAAGAGGACACCTC 312
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428 ATTCTCTCTACACCTGCTATCTTCCACCATTAAGGCAATTCGTAACCTGGAACATG 487
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313 ATTCTCTCTACACCTGCTATCTTCCACCATTAAGGCAATTCGTAACCTGGAACATG 372
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488 AAGGAGCGCTGTGTGATCCGGGCTGTGAGAAACAGAGTGGTATCTACTCTCTCTACATCA 547
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373 AAGGAGCGCTGTGTGATCCGGGCTGTGAGAAACAGAGTGGTATCTACTCTCTCTACATCA 432
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548 GCGTATGATGCTGCGGCCAGGGGCTCAACACACTGTTGGCTAAAGGGCTTGAGCTTGT 607
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433 GCGTATGATGCTGCGGCCAGGGGCTCAACACACTGTTGGCTAAAGGGCTTGAGCTTGT 492
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608 ACGTCAGGCGCATATCTCTCCCAAGCTCCCACTACCTCTACAGAGGAAACACACCA 667
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493 ACGTCAGGCGCATATCTCTCCCAAGCTCCCACTACCTCTACAGAGGAAACACACCA 552
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668 GTGAATTCACGTTAACTACACCAAGACTGAGCAAAAGTCTGTCGAGTGAAGA 727
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553 GTGAATTCACGTTAACTACACCAAGACTGAGCAAAAGTCTGTCGAGTGAAGA 612
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728 ATTGACGGTGTCTGTCACTTCTTTTCTGTAGAGCTGTGTAATGAGAAACAACACGG 787
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613 ATTGACGGTGTCTGTCACTTCTTTTCTGTAGAGCTGTGTAATGAGAAACAACACGG 672
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788 ATTAATCTGAATGTCTCAGAAAGGCTTGATGAGAGTGTGTAATTTCTTCCCGGAAC 847
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673 ATTAATCTGAATGTCTCAGAAAGGCTTGATGAGAGTGTGTAATTTCTTCCCGGAAC 732
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848 AAACAACCTTATCAGAGAGCAAAATCTGTCACTGAGAGAGCTTGTGCTTACATAC 907
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733 AAACAACCTTATCAGAGAGCAAAATCTGTCACTGAGAGAGCTTGTGCTTACATAC 792
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908 GGAATGGAGAGGTTATGACACACTGATGATCTGTCTCCCTGGCAACATGATGATGCA 967
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793 GGAATGGAGAGGTTATGACACACTGATGATCTGTCTCCCTGGCAACATGATGATGCA 852
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968 ATTAAGAGACACCTAAACATATCTCATATTCGCTTAGCCCTTGCGGTGGGAGAACCTTA 1027
|||||

Db 853 ATTAAGAGACACCTAAACATATCTCATATTCGCTTAGCCCTTGCGGTGGGAGAACCTTA 912
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QY 1028 GAGTCTCAAGTCAAACTC 1045
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Db 913 GAGTCTCAAGTCAAACTC 930
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RESULT 2
BU172435 857 bp mRNA linear EST 04-SEP-2002
LOCUS AGENCOURT_7970438 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6164871
DEFINITION 5', mRNA sequence.
ACCESSION BU172435
VERSION BU172435.1 GI:22686419
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 857)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
CONTACT: Robert Strausberg, Ph.D.
COMMENT Email: cga@pds-remail.nih.gov
Tissue Procurement: ATCC/DCPD/DP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
plate: L1AM13522 row: k column: 16
High quality sequence stop: 728.

FEATURES
source
1. .857
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6164871"
/issue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."

BASE COUNT 234 a 201 c 199 g 223 t

Query Match 53.6%; Score 833; DB 13; Length 857;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

492 AGCGCTGTGATCCGGGCTGTGAGAAACAGAGTGGTATCTCTCTCATACAGCT 551
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1 AGCGCTGTGATCCGGGCTGTGAGAAACAGAGTGGTATCTCTCTCATACAGCT 60
|||||
552 ATGATGCTGCGGCCAGGGGCTCAACACTGTTGGCTAAAGGGCTTGAGCTTGA 611
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61 ATGATGCTGCGGCCAGGGGCTCAACACTGTTGGCTAAAGGGCTTGAGCTTGA 120
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612 CCAAGCCATATCTCTCCAAAGCTCCCACTACCTACAGAGGAAACACCGAGTAG 671
|||||
121 CCAAGCCATATCTCTCCAAAGCTCCCACTACCTACAGAGGAAACACCGAGTAG 180
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672 AATTCAAGCTTAACACCAACAGCTGAGCAAAAGTCAATGTCTGCAATGAAAGATTG 731
|||||
181 AATTCAAGCTTAACACCAACAGCTGAGCAAAAGTCAATGTCTGCAATGAAAGATTG 240
|||||
732 ACGGTGTTCTGTCACTTCTTTTCTGTGAGAGCTGTATGAGAAACAACGAGATT 791
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Db	241	ACGGTGTTCGTCACTCTTTTCTGCTAGACGCTGTAATGAGAAACAAC	CAOGANTTA	300
Qy	792	ATCTGAATGTGACTCAGAAAGCCTTGATGCAAGGTGATGATTTCTTCCGGAACAAC	851	
Db	301	ATCTGAATGTGACTCAGAAAGCCTTGATGCAAGGTGATGATTTCTTCCGGAACAAC	360	
Qy	852	AACCTTATCAACAAGCGAAATTCGTGACAGGGAAGCCCTTGCTTCAATACTGGAA	911	
Db	361	AACCTTATCAACAAGCGAAATTCGTGACAGGGAAGCCCTTGCTTCAATACTGGAA	420	
Qy	912	TGGGACGGTATTCACACACTGTGATGAATCTGCTCCCTGGCAACATGATTCAGTAATPA	971	
Db	421	TGGGACGGTATTCACACACTGTGATGAATCTGCTCCCTGGCAACATGATTCAGTAATPA	480	
Qy	972	AAAGACACCTTAAACTATCTATATTCGCTTAGCCCTTGGGTGGGGAGAACTTGAAGT	1031	
Db	481	AAAGACACCTTAAACTATCTATATTCGCTTAGCCCTTGGGTGGGGAGAACTTGAAGT	540	
Qy	1032	CTCAAGTCAAAAGTGTGGCCCTGTGTGCTGGTTCTGGAGCAGCGTTCTGCAGGGGTGG	1091	
Db	541	CTCAAGTCAAAAGTGTGGCCCTGTGTGCTGGTTCTGGAGCAGCGTTCTGCAGGGGTGG	600	
Qy	1092	AGGCTGACCTTACTCTACACAGGTGAGATGTCCTCATGATTAATCTTGGATGCTGCTCC	1151	
Db	601	AGGCTGACCTTACTCTACACAGGTGAGATGTCCTCATGATTAATCTTGGATGCTGCTCC	660	
Qy	1152	AAGGAATTAATGTGATCTCTGTGTGAACAACAGCAACACTGAAGAGGCTTCTTCTGACC	1211	
Db	661	AAGGAATTAATGTGATCTCTGTGTGAACAACAGCAACACTGAAGAGGCTTCTTCTGACC	720	
Qy	1212	TTTCAGATATCTGTGATTTCTCACTTGGAGAAATTAATTAATTAATCTTCAAGAGACTG	1271	
Db	721	TTTCAGATATCTGTGATTTCTCACTTGGAGAAATTAATTAATTAATCTTCAAGAGACTG	780	
Qy	1272	ACAGGAGACCCCTCTCAGGTGTTAATTAATTCAGAAACATCAGAGATTAACCATTC	1324	
Db	781	ACAGGAGACCCCTCTCAGGTGTTAATTAATTCAGAAACATCAGAGATTAACCATTC	833	
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LOCUS	AL581997	1201 bp	mRNA	linear
DEFINITION	AL581997 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED			
ACCESSION	AL581997			
VERSION	AL581997.2	GI:31320228		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.			
TITLE	Full-length cDNA libraries and normalization			
JOURNAL	Unpublished			
COMMENT	On Feb 16, 2001 this sequence version replaced gi:12949550.			
	Contact: Genoscope			
	Genoscope - Centre National de Sequencage			
	BP 191 91006 Evry cedex - France			
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr			
	Library was constructed by Life Technologies, a division of			
	Invitrogen. This sequence belongs to sequence cluster 1287.f. For			
	more information about this cluster, see			
	http://www.genoscope.cns.fr/			
	cgl-bin/cluster.cgi?seq=CS0DL003BD12QPl&cluster=1287.f. Contact :			
	Feng Liang Email : fliang@lifetech.com URL :			
	http://fulllength.invitrogen.com/ Invitrogen Corporation 1600			
	Faraday Avenue Genoscope sequence ID : CS0DL003BD12QPl.			
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/cell_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      293 a      286 c      277 g      310 t      35 others
ORIGIN

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Query Match	53.38;	Score 827;	DB 9;	Length 1201;
Best Local Similarity	100.08;	Pred. No. 0;		
Matches 827;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

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Db	115	AGTCCCAAGACAGTCGCGGTTTGATGATTCCTCGATCTCAATCTTCCGCTCTCAT	174
OY	247	GGATTGGAAGGCTCTTCCTTCTTCTCTGATGACTTTCATCCCTCTCGTTGCTAGAG	306
Db	175	GGATTGGAAGGCTCTTCCTTCTTCTCTGATGACTTTCATCCCTCTCGTTGCTAGAG	234
OY	307	TTGGACATGTTGGATTACTGCTGGAACCAAGCCACACACTACTGTAATACACTCTT	366
Db	235	TTGGACATGTTGGATTACTGCTGGAACCAAGCCACACACTACTGTAATACACTCTT	294
OY	367	CCTGACCAATGACTGCTAGAGAAAGTATGGAGAGGTCTGCAAAAGAGCAGACCT	426
Db	295	CCTGACCAATGACTGCTAGAGAAAGTATGGAGAGGTCTGCAAAAGAGCAGACCT	354
OY	427	CATTCTGCTCAATCCGCGCTATCTTCGACCACGAAGCGGATACCTGGAAACATG	486
Db	355	CATTCTGCTCAATCCGCGCTATCTTCGACCACGAAGCGGATACCTGGAAACATG	414
OY	487	GAAGAGCGCGCTGTGTATCCGGGCTCTGGAGAACAGAGTCGGTATCTCTCTATAC	546
Db	415	GAAGAGCGCGCTGTGTATCCGGGCTCTGGAGAACAGAGTCGGTATCTCTCTATAC	474
OY	547	AGCCTATGATGTGTGGGCCCCAGAGGGGTCAAAACACTGGTGGCTAAAGGGCTTGAGACTTG	606
Db	475	AGCCTATGATGTGTGGGCCCCAGAGGGGTCAAAACACTGGTGGCTAAAGGGCTTGAGACTTG	534
OY	607	TACCTCAGGGCCATACATCTCTTCAMAAAGCTCCCAACTACCCCTACAGAGAGGAACCCAGC	666
Db	535	TACCTCAGGGCCATACATCTCTTCAMAAAGCTCCCAACTACCCCTACAGAGAGGAACCCAGC	594
OY	667	AGTACAATTCAACGTTAACTACACCCAGAAGCTGGACAAAGTCATGTCTGCACTGAAGG	726
Db	595	AGTACAATTCAACGTTAACTACACCCAGAAGCTGGACAAAGTCATGTCTGCACTGAAGG	654
OY	727	AATTGACGGTGTCTGTGACTCTTCTTCTCTAGAGACTGGTAATGAGAGAACAAACAGC	786
Db	655	AATTGACGGTGTCTGTGACTCTTCTTCTCTAGAGACTGGTAATGAGAGAACAAACAGC	714
OY	787	GATTATCTGAATTGTACTCAGAGGCTTGTGATGCAAGGTGTAGATTTTCTTCCGGAA	846
Db	715	GATTATCTGAATTGTACTCAGAGGCTTGTGATGCAAGGTGTAGATTTTCTTCCGGAA	774
OY	847	CAAAACAACCTTTCAGAAAGAGGAATTCGTACATGGAGAAAGCCCTTCTCTACATAC	906
Db	775	CAAAACAACCTTTCAGAAAGAGGAATTCGTACATGGAGAAAGCCCTTCTCTACATAC	834
OY	907	TGGAATGGAGCGTTATGACACTGGATGAATCTGTCTCCCTGGCAACATGATTTATCG	966
Db	835	TGGAATGGAGCGTTATGACACTGGATGAATCTGTCTCCCTGGCAACATGATTTATCG	894
OY	967	AATAAAGACACCTTAAACCTATCTCATATTCGCTTAGCCCTTGGGG	1013
Db	895	AATAAAGACACCTTAAACCTATCTCATATTCGCTTAGCCCTTGGGG	941

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RESULT 4
LOCUS      BX446370
DEFINITION BX446370 Homo sapiens PLACENTA Homo sapiens cDNA clone CLOB0042B11
ACCESSION  BX446370
VERSION     BX446370.1
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   1 (bases 1 to 1201)
AUTHORS    Li, W.-B., Gruber, C., Jesse, J., and Polayes, D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL    Unpublished
COMMENT     Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
            Library was constructed by life technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 1287.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CLOB0042B11&cluster=1287.f. Contact :
            Feng Liang Email: fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/Invitrogen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CLOB0042B11RP1.
            Location/Qualifiers
                1..1201
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                /db_xref="taxon:9606"
                /clone="CLOB0042B11"
                /issue_type="PLACENTA"
                /clone_lib="Homo sapiens PLACENTA"
                /note="Vector: pCMVSPORT.6; 1st strand cDNA was primed
                with a NotI-oligo(dT) primer. Five prime end enriched,
                double-strand cDNA was digested with Not I and cloned into
                the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                Library was not normalized."
BASE COUNT 349 a 256 c 266 g 296 t 34 others
ORIGIN
Query Match 52.0%; Score 808; DB 13; Length 1201;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 858; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 389 GAAGTATGAGAGAGTGTGCAAAAGAGGCGAGACCTCATTTCTCTACCATCCGCT 448
DB |||||||
DB 70 GAAGTATGAGAGAGTGTGCAAAAGAGGCGAGACCTCATTTCTCTACCATCCGCT 129
QY 449 ATCTTCGACCATGAGGCGATACCTGGAACACATGGAAGAGGCGCTGGATCCG 508
DB |||||||
DB 130 ATCTTCGACCATGAGGCGATACCTGGAACACATGGAAGAGGCGCTGGATCCG 189
QY 509 GCTGTGAGAGAGAGTGTGCAAAAGAGGCGAGACCTCATTTCTCTACCATCCG 568
DB |||||||
DB 190 GCTGTGAGAGAGAGTGTGCAAAAGAGGCGAGACCTCATTTCTCTACCATCCG 249
QY 569 GCGGTACACACTGGTGGCTAAAGGGCTTGAAGCTTGACCTCCAGGCCCATACACT 628
DB |||||||
DB 250 GCGGTACACACTGGTGGCTAAAGGGCTTGAAGCTTGACCTCCAGGCCCATACACT 309
QY 629 TCCTAAGCTCCACACTACCTACAGAGGGAACCCAGGAGTGAATCAACCTTACTAC 688
DB |||||||
DB 310 TCCTAAGCTCCACACTACCTACAGAGGGAACCCAGGAGTGAATCAACCTTACTAC 369
QY 689 ACCCAAGACCTGAGCAAACTCATGTCTGCAGTGAAGAAATTGACGCTTTCTGACAT 748
DB |||||||
DB 370 ACCCAAGACCTGAGCAAACTCATGTCTGCAGTGAAGAAATTGACGCTTTCTGACAT 429
QY 749 TCTTTTCTGCTAGAGACTGTAATGAGAACAAACAGGATTAATCTGAATTGACTCAG 808

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DB |||||||
QY 430 TCTTTTCTGCTAGAGACTGTAATGAGAACAAACGATTAATCTGAATTGACTCAG 489
QY 809 AAGGCTTATGACAGTGTAGATTTTCTTCCCGAACAACACTTATCAGAAAGC 868
DB |||||||
DB 490 AAGGCTTATGACAGTGTAGATTTTCTTCCCGAACAACACTTATCAGAAAGC 549
QY 869 GAAATTCGTCACTGAGAGAGCCTTGTCTTACATCTGGAATGGAGCGTTATGACACA 928
DB |||||||
DB 550 GAAATTCGTCACTGAGAGAGCCTTGTCTTACATCTGGAATGGAGCGTTATGACACA 609
QY 929 CTGATGATCTGTCTCCCGCAACCATGATGATGATTAAGAACACCTTAACATA 988
DB |||||||
DB 610 CTGATGATCTGTCTCCCGCAACCATGATGATGATTAAGAACACCTTAACATA 669
QY 989 TCTCATATTCGCTTACCCCTTGGGCTGGGAGAGACCTTACAGTCAAGTCAAGTCGTG 1048
DB |||||||
DB 670 TCTCATATTCGCTTACCCCTTGGGCTGGGAGAGACCTTACAGTCAAGTCAAGTCGTG 729
QY 1049 GCCCTGTGTGCTGTGCTGTGAGAGACAGCTTGTGACAGGCTGTGAGGCTTACCTTC 1108
DB |||||||
DB 730 GCCCTGTGTGCTGTGCTGTGAGAGACAGCTTGTGACAGGCTGTGAGGCTTACCTTC 789
QY 1109 ACAAGTGAATGCTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1168
DB |||||||
DB 790 ACAAGTGAATGCTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 849
QY 1169 CTCTGTGAACACAGCAACTGACAGAGGCTTCTTCTGACCTTCGAGATATGCTGAT 1228
DB |||||||
DB 850 CTCTGTGAACACAGCAACTGACAGAGGCTTCTTCTGACCTTCGAGATATGCTGAT 909
QY 1229 TCTCACTTGAGATATAGA 1247
DB |||||||
DB 910 TCTCACTTGAGATATAGA 928

RESULT 5
LOCUS      AL521920
DEFINITION AL521920 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
ACCESSION  AL521920
VERSION     AL521920.2
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   1 (bases 1 to 957)
AUTHORS    Li, W.-B., Gruber, C., Jesse, J., and Polayes, D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL    Unpublished
COMMENT     On Feb. 13, 2001 this sequence version replaced g1:12785413.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
            Library was constructed by life technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 1287.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DB003DH07QPI&cluster=1287.f. Contact :
            Feng Liang Email: fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/Invitrogen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DB003DH07QPI.
            Location/Qualifiers
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                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="CS0DB003YPI4"
                /issue_type="NEUROBLASTOMA COT 10-NORMALIZED"
                /clone_lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"

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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 250 a 239 c 217 g 250 t 1 others

Query Match 50.7%; Score 787; DB 9; Length 957;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 787; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

187 AGTCCCGACGACAGTCCGGTTGTAGATTCCTGATTCGATTCCTTCCTTCAT 246
108 AGTCCCGACGACAGTCCGGTTGTAGATTCCTGATTCGATTCCTTCCTTCAT 167
247 GGATTTGAAGGCT 306
168 GGATTTGAAGGCT 227
307 TTGGACAAATGTTGGATTACTGTGTGAACCAAGCCCAACATCTGTAATACACT 366
228 TTGGACAAATGTTGGATTACTGTGTGAACCAAGCCCAACATCTGTAATACACT 287
367 CTTGACCAATGCTGACTGAGAGAGTGTGAGAGAGTGTGCAAAAAGAGGACACT 426
288 CTTGACCAATGCTGACTGAGAGAGTGTGAGAGAGTGTGCAAAAAGAGGACACT 347
427 CATTCCTCCACATCCGCTATCTCTCCGACCCATGAAAGGCAATACCTGAACTG 486
348 CATTCCTCCACATCCGCTATCTCTCCGACCCATGAAAGGCAATACCTGAACTG 407
487 GAAGAGAGGCTGTGTGATCCGGCTCTGTGAACAGAGTGGTATCTCTCTCTATC 546
408 GAAGAGAGGCTGTGTGATCCGGCTCTGTGAACAGAGTGGTATCTCTCTCTATC 467
547 AGCCTATGATCTGTGCGCCCAAGGCGTCAACACTGTTGGCTAAAGGCTTGAAGCT 606
468 AGCCTATGATCTGTGCGCCCAAGGCGTCAACACTGTTGGCTAAAGGCTTGAAGCT 527
607 TACCTCCAGGCGCATACATCTCTCCAAAGCTCCCAACCTACAGAGGAAACACAGC 666
528 TACCTCCAGGCGCATACATCTCTCCAAAGCTCCCAACCTACAGAGGAAACACAGC 587
667 AGTGAATTCACAGTTAATCACTACACCAAGACCTGTGACAAAGTCACTGTGTAAGG 726
588 AGTGAATTCACAGTTAATCACTACACCAAGACCTGTGACAAAGTCACTGTGTAAGG 647
727 AATTGACGGTCTTCTGCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 786
648 AATTGACGGTCTTCTGCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 707
787 GATTAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 846
708 GATTAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 767
847 CAACCAACTTTATCAGAAAGAGGAAATCTGTCACTGAGAGACCTTTCTCTCTATAC 906
768 CAACCAACTTTATCAGAAAGAGGAAATCTGTCACTGAGAGACCTTTCTCTCTATAC 827
907 TGGAAATGGAGGTTTATGACACATGAGATGTAATCTGTCTCCCTGGCAACATGATGATG 966
828 TGGAAATGGAGGTTTATGACACATGAGATGTAATCTGTCTCCCTGGCAACATGATGATG 887
967 AATAAAA 973
888 AATAAAA 894

RESULT 6
BM545164
LOCUS
DEFINITION
BM545164 1117 bp mRNA linear EST 20-FEB-2002
AGENCOURT_6497453 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:558980
5', mRNA sequence.

ACCESSION BM545164
VERSION BM545164.1 GI:18777026
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS NIH-MGC
TITLE NIH-MGC
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: c99abs-r@mail.nih.gov
Tissue Procurement: Invitrogen

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed By: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: LHAM12360 row: p column: 05
High quality sequence stop: 734.
Location/Qualifiers

FEATURES
source 1..1117
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:558980"
/lab_host="DH10B"
/clone_11b="NIH-MGC_125"

/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site:1: EcoRV (destroyed); Site:2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb. Insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."

BASE COUNT 278 a 282 c 260 g 293 t 4 others

Query Match 50.5%; Score 784; DB 12; Length 1117;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 784; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

188 GTCCCGACGACAGTCCGGTTGTAGATTCCTGATTCGATTCCTTCCTTCATG 247
31 GTCCCGACGACAGTCCGGTTGTAGATTCCTGATTCGATTCCTTCCTTCATG 90
248 GATTGAAGGCT 307
91 GATTGAAGGCT 150
308 TGGCAATGTTGATTAATCACTACACCAAGACCTGTGACAAAGTCACTGTAATAC 367
151 TGGCAATGTTGATTAATCACTACACCAAGACCTGTGACAAAGTCACTGTAATAC 210
368 CTGACCAATGACCTGACAGAGAGTGTGAGAGAGTGTGCTCAAAAGAGCAACCTC 427
211 CTGACCAATGACCTGACAGAGAGTGTGAGAGAGTGTGCTCAAAAGAGCAACCTC 270
428 ATTCTCTCTACCACTGCGCTATCTCTCGACCAATGAAAGCGATTAACCTGGAACATG 487
271 ATTCTCTCTACCACTGCGCTATCTCTCGACCAATGAAAGCGATTAACCTGGAACATG 330
488 AAGGAGCGCTGTGTGATCCGGCTCTGTGAGACAGAGTGTGATCTCTCTCTATACA 547
331 AAGGAGCGCTGTGTGATCCGGCTCTGTGAGACAGAGTGTGATCTCTCTCTATACA 390
548 GCTATGATGCTGTGCGCCCAAGGCGTCAACAACTGTTGGCTAAAGGCTTGAAGCTTGT 607
391 GCTATGATGCTGTGCGCCCAAGGCGTCAACAACTGTTGGCTAAAGGCTTGAAGCTTGT 450

```

QY 608 ACCGCCAGGCCATACATCTCTCCAAAGCTCCCACTACCTACAGAGGGAACACCGA 667
DB 451 ACCTCAGGCCATACATCTCTCCAAAGCTCCCACTACCTACAGAGGGAACACCGA 510
QY 668 GTAGAAATTAAGCTTAACACACCCAGACCTGGACAAAGTATGTCTGACATGAAGA 727
DB 511 GTAGAAATTAAGCTTAACACACCCAGACCTGGACAAAGTATGTCTGACATGAAGA 570
QY 728 ATTGACGGTGTCTCTGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 787
DB 571 ATTGACGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 630
QY 788 ATTAATCTGAATTTGATCTGAGAGGCTTTGATGACAGTGTATGATTTCTTCCCGAAC 847
DB 631 ATTAATCTGAATTTGATCTGAGAGGCTTTGATGACAGTGTATGATTTCTTCCCGAAC 690
QY 848 AAACAATCTTATCAGAGAGGAAATTTGCTGCTGACAGAGAGGCTTTGCTTCTACTACT 907
DB 691 AAACAATCTTATCAGAGAGGAAATTTGCTGCTGACAGAGAGGCTTTGCTTCTACTACT 750
QY 908 GGAATGGAGCGGTATGACACACTGATGATCTGCTCCCTGGCAACATGATGATGCA 967
DB 751 GGAATGGAGCGGTATGACACACTGATGATCTGCTCCCTGGCAACATGATGATGCA 810
QY 968 ATAA 971
DB 811 ATAA 814

RESULT 7
LOCUS BQ229243 836 bp mRNA linear EST 02-MAY-2002
DEFINITION AGENCOURT 7510797 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6055256
5', mRNA sequence.
ACCESSION BQ229243
VERSION BQ229243.1 GI:20410643
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 836)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC/DC/DTP
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM13315 row: f column: 01
High quality sequence stop: 677.
Location/Qualifiers
1. 836
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/clone="IMAGE:6055256"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: Skin; Vector: PCMV-SpOrf6; Site:1: NCI;
Site:2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
BASE COUNT 218 a 205 c 200 g 211 t 2 others
ORIGIN

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Query Match 49.5%; Score 769; DB 13; Length 836;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 769; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 TTGAAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 309
DB 1 TTGAAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
QY 310 GGCAATGTGTGATTTACTGTTGAGAACCAAGCCACACATCTGTAAATACATCTCTCT 369
DB 61 GGCAATGTGTGATTTACTGTTGAGAACCAAGCCACACATCTGTAAATACATCTCTCTCT 120
QY 370 GACCAATGACCTGACAGAGAGTATGAGAGGCTCTGCAAGAGGACAGCTCAT 429
DB 121 GACCAATGACCTGACAGAGAGTATGAGAGGCTCTGCAAGAGGACAGCTCAT 180
QY 430 TCTCTCTCAACATCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 489
DB 181 TCTCTCTCAACATCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 490 GGAAGCGCTGTGATCCGGGCTCTGGAAGACAGATCGTATCTACTCTCTCTCTCTCTCT 549
DB 241 GGAAGCGCTGTGATCCGGGCTCTGGAAGACAGATCGTATCTACTCTCTCTCTCTCTCT 300
QY 550 CTATGATGCTGCGCCCGCCAGGCGCTCAACAATGCTGCTAAAGGCTTGGAGCTGTAC 609
DB 301 CTATGATGCTGCGCCCGCCAGGCGCTCAACAATGCTGCTAAAGGCTTGGAGCTGTAC 360
QY 610 CTCGAGGCCATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 669
DB 361 CTCGAGGCCATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
QY 670 AGAATTCACAGTTTACTACACCCAGACCTGACAAAGTCTGCTGACAGTAAAGAA 729
DB 421 AGAATTCACAGTTTACTACACCCAGACCTGACAAAGTCTGCTGACAGTAAAGAA 480
QY 730 TGACGGTGTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 789
DB 481 TGACGGTGTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
QY 790 TAATCTGAATTTGATCTGAGAGGCTTTGATGACAGGCTGATTTCTTCCCGAACAA 849
DB 541 TAATCTGAATTTGATCTGAGAGGCTTTGATGACAGGCTGATTTCTTCCCGAACAA 600
QY 850 ACAACTTATCAGAGAGGAAATTTGCTGCTGAGAGAGGCTTTGCTTCTACTACTCTG 909
DB 601 ACAACTTATCAGAGAGGAAATTTGCTGCTGAGAGAGGCTTTGCTTCTACTACTCTG 660
QY 910 AATGGAGCGTTATGACACACTGATGATGTCTCTCTGGAACCATGATTTGAAAT 969
DB 661 AATGGAGCGTTATGACACACTGATGATGTCTCTCTGGAACCATGATTTGAAAT 720
QY 970 AAAAAGACACCTTAAATCTATCTGCTTACGCTTGGGCTGGG 1018
DB 721 AAAAAGACACCTTAAATCTATCTGCTTACGCTTGGGCTGGG 769

RESULT 8
LOCUS AL529615 1201 bp mRNA linear EST 23-MAY-2003
DEFINITION AL529615 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
cDNA clone CS0DD006YH18 5-PRIME, mRNA sequence.
ACCESSION AL529615
VERSION AL529615.2 GI:31067458
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1201)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC/DC/DTP
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM13315 row: f column: 01
High quality sequence stop: 677.
Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: Skin; Vector: PCMV-SpOrf6; Site:1: NCI;
Site:2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
BASE COUNT 218 a 205 c 200 g 211 t 2 others
ORIGIN

```

COMMENT On Feb 13, 2001 this sequence version replaced g1:12793108.
 Contact: Genoscope
 Genoscope - Centre National de Sequenage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 1287.f For more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DD006DD09Qp1&cluster=1287.f. Contact :
 Peng Liang Email : filiang@life.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DD006DD09QF1.
 Location/Qualifiers
 1. 1201

FEATURES
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DD006YH18"
 /tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT 319 a 286 c 274 g 299 t 23 others

ORIGIN

Query Match 49.1%; Score 763; DB 9; Length 1201;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 913; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

203 CGGTTTGTAGATTCCTGATCTGCAATTCCTCCGTTCCCTTCAATGATTTGAAGGCTC 262
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 Db 129 CGGTTTGTATATCCCGATCTGCAATTCCTCCGTTCCCTTCAATGATTTGAAGGCTC 188
 |||||||
 Qy 263 CTTTCTTCTTGAATGATTCGATTCCTCTGTTTCTGAGATTTGGACAAATTTGA 322
 |||||||
 Db 189 CTTTCTTCTTGAATGATTCGATTCCTCTGTTTCTGAGATTTGGACAAATTTGA 248
 |||||||
 Qy 323 TTACTGTGAGACCAACCCACACATACCTTAATACCTTCCCGACCAATGACCTG 382
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 Db 249 TTACTGTGAGACCAACCCACACATACCTTAATACCTTCCCGACCAATGACCTG 308
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 Qy 383 ACTGAGAGATGATGAGAGAGTGTCTCAAAAGAGAGACGATTCCTCTTACCAT 442
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 Db 309 ACTGAGAGATGATGAGAGAGTGTCTCAAAAGAGAGACGATTCCTCTTACCAT 368
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 Qy 443 CCGCTATCTTCGAGACCATGAAGCGCATAACTGGAACACATGGAAGACCGCTGTG 502
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 Db 369 CCGCTATCTTCGAGACCATGAAGCGCATAACTGGAACACATGGAAGACCGCTGTG 428
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 Qy 503 ATCCGGGCTCTGGAACACAGTGGTATCTACTCTCTCTATACAGCTTAAGTGTGG 562
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 Db 429 ATCCGGGCTCTGGAACACAGTGGTATCTACTCTCTCTATACAGCTTAAGTGTGG 488
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 Qy 563 CCCAGAGGCGTCAACAACGTTGGCTAAAGGGCTTGAGCTTACCTCAGGCCATA 622
 |||||||
 Db 489 CCCAGAGGCGTCAACAACGTTGGCTAAAGGGCTTGAGCTTACCTCAGGCCATA 548
 |||||||
 Qy 623 CATCTTTCACAAAGCTCCCACTACAGAGAGGAAACACAGTGAATTAAGCTT 682
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 Db 549 CATCTTTCACAAAGCTCCCACTACAGAGAGGAAACACAGTGAATTAAGCTT 608
 |||||||
 Qy 683 AACTACACCAAGACCTGGAACAGTATGTCTGCAATGAAAGAAATGAGCTTTCT 742
 |||||||
 Db 609 AACTACACCAAGACCTGGAACAGTATGTCTGCAATGAAAGAAATGAGCTTTCT 668
 |||||||
 Qy 743 GTCACTTCTTTCTGTAGACTGTAATGAGGAAACAAAGGATTAATCTGAATGT 802
 |||||||
 Db 669 GTCACTTCTTTCTGTAGACTGTAATGAGGAAACAAAGGATTAATCTGAATGT 728
 |||||||
 Qy 803 ACTCAGAGGCTTTGATGAGGTGTAGATTTCTTCCCGAACAACACTTATCAG 862

Db 729 ACTCAGAGGCTTTGATGAGGTGTAGATTTCTTCCCGAACAACACTTATCAG 788
 |||||||
 Qy 863 AAGACGGAATTCGTCTACTGAGAGAGCCTTCTTCTTACTACTGAGAGAGCTTA 922
 |||||||
 Db 789 AAGACGGAATTCGTCTACTGAGAGAGCCTTCTTCTTACTACTGAGAGAGCTTA 848
 |||||||
 Qy 923 TGCACACTGATGATGATGCTGCTCCCTGGCAACATGATGCAATTAAGACACTA 982
 |||||||
 Db 849 TGCACACTGATGATGATGCTGCTCCCTGGCAACATGATGCAATTAAGACACTA 908
 |||||||
 Qy 983 AAATATCTCATATTCGCTTATGACCTTGGGGTGGGAGAACCTTAGACTCTCAAGTCAA 1042
 |||||||
 Db 909 AAATATCTCATATTCGCTTATGACCTTGGGGTGGGAGAACCTTAGACTCTCAAGTCAA 968
 |||||||
 Qy 1043 GTCTGGGCGCTGTGTGCTGCTTCTGAGAGAGAGCCTTCTGAGAGGTGTGAGAGCTT 1102
 |||||||
 Db 969 GTCTGGGCGCTGTGTGCTGCTTCTGAGAGAGAGCCTTCTGAGAGGTGTGAGAGCTT 1028
 |||||||
 Qy 1103 TACCTCAGAGGTGAGA 1118
 |||||||
 Db 1029 TACCTCAGAGGTGAGA 1044
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RESULT 9 929 bp mRNA linear EST 16-OCT-2002
 B0859307
 LOCUS
 DEFINITION AGENCOURT_10422791 NIH_MGC_109 Homo sapiens cDNA clone
 IMAGE:6650148 5', mRNA sequence.
 ACCESSION B0859307
 VERSION B0859307.1 GI:24044299.
 KEYWORDS EST.
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 929)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMU at:
 http://image.llnl.gov
 Plate: L1CM2894 row: 0 column: 12
 High quality sequence stop: 754.
 Location/Qualifiers
 1. 929

FEATURES
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 /clone="IMAGE:6650148"
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 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_109"
 /note="Organ: ovary; Vector: pOT87; Site:1: EcoRI; Site:2:
 XhoI; cDNA made by oligo-dT priming. directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCAAGAG(G). Library constructed by Ling Hong in the
 Laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

BASE COUNT 251 a 212 c 218 g 247 t 1 others

ORIGIN

Query Match 47.1%; Score 732; DB 13; Length 929;
 Best Local Similarity 99.8%; Pred. No. 0;

Matches	832;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
QY	491	GAGCGCTGCTGATCCGGCTCTGAGAACAGAGTGGATCTCTCTCTCTACAGCC	550	1	GAGCGCTGCTGATCCGGCTCTGAGAACAGAGTGGATCTCTCTCTCTACAGCC	60			
QY	551	TATGATGCTGCGCCCGAGGCGCTCAACAAGTGGTGGTAAAGGCTTGGAGCTTAC	610	61	TATGATGCTGCGCCCGAGGCGCTCAACAAGTGGTGGTAAAGGCTTGGAGCTTAC	120			
QY	611	TCGAGGCCATCATCCTTCCAAAGCTCCCAATACCTCTACAGAGGAAACCCAGTA	670	121	TCGAGGCCATCATCCTTCCAAAGCTCCCAATACCTCTACAGAGGAAACCCAGTA	180			
QY	671	GATTCACAGTTAACTACACACCAAGAGCTGAGCAAGTATGCTCAGTGAAGAAAT	730	181	GATTCACAGTTAACTACACACCAAGAGCTGAGCAAGTATGCTCAGTGAAGAAAT	240			
QY	731	GACGCTGTTCTGCTCACTCTTTTCTGCTAGAGCTGTAATGAGAACAAACAGGAT	790	241	GACGCTGTTCTGCTCACTCTTTTCTGCTAGAGCTGTAATGAGAACAAACAGGAT	300			
QY	791	AATCTGAATTTGATACAGAAAGGCTTATGAGAGAGTGGTATGCTTCTCCGAGCAAA	850	301	AATCTGAATTTGATACAGAAAGGCTTATGAGAGAGTGGTATGCTTCTCCGAGCAAA	360			
QY	851	CACTTTATCAGAAAGAGAAATTCCTGCTAGTGAAGAGCTTCTGCTACATCTGA	910	361	CACTTTATCAGAAAGAGAAATTCCTGCTAGTGAAGAGCTTCTGCTACATCTGA	420			
QY	911	ATGGGAGCTTATGACACATGATGATGCTCTCTCTGCAACATGATGATGAAT	970	421	ATGGGAGCTTATGACACATGATGATGCTCTCTCTGCAACATGATGATGAAT	480			
QY	971	AAAAGACACTTAAATATCTATCTATCTGCTTACGCTTGGGGTGGGAGAACTTAG	1030	481	AAAAGACACTTAAATATCTATCTATCTGCTTACGCTTGGGGTGGGAGAACTTAG	540			
QY	1031	TCCTCAAGTCAAAAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1090	541	TCCTCAAGTCAAAAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	600			
QY	1091	GAGGCGACCTTACCTCAGAGTGAAGTGGTGGGAGAGCTTCTGCAAGGCTT	1150	601	GAGGCGACCTTACCTCAGAGTGAAGTGGTGGGAGAGCTTCTGCAAGGCTT	660			
QY	1151	CAAGGAATTAATGTCTCTCTGTAACAGACAGCACTGAAGAGCTTCTTCTGAC	1210	661	CAAGGAATTAATGTCTCTCTGTAACAGACAGCACTGAAGAGCTTCTTCTGAC	720			
QY	1211	CTTCGAGATATGCTGATTCCTCACTGGAATTAATTAATTAATTAATTAATTAAT	1270	721	CTTCGAGATATGCTGATTCCTCACTGGAATTAATTAATTAATTAATTAATTAAT	780			
QY	1271	GACAGGAGCCCTTCTCAGTGGTATTAATGAGAAACATCAGATTAACATTC	1324	781	GACAGGAGCCCTTCTCAGTGGTATTAATGAGAAACATCAGATTAACATTC	834			
RESULT 10	BM557530	1019 bp	mRNA	linear	EST 20-FEB-2002				
LOCUS	BM557530								
DEFINITION	AGENCOUT_6563433 NIH_MGC_88 Homo sapiens cDNA IMAGE:5739935								
ACCESSION	BM557530								
VERSION	BM557530.1								
KEYWORDS	EST.								
SOURCE	Homo sapiens (human)								
ORGANISM	Homo sapiens								
REFERENCE	1 (bases 1 to 1019)								
AUTHORS	NIH-MGC http://mhc.ncl.nih.gov/.								

TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgrabs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL) Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLNL2754 row: a column: 24 High quality sequence stop: 685. Location/Qualifiers 1. 1019 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5739935" /issue_type="duodenal adenocarcinoma, cell line" /lab_host="PH10B (phage-resistant)" /clone_lib="NIH_MGC_88" /note="Organ: small intestine; Vector: pCMV-Sport6; Site_1: Not; Site_2: Salt; Cloned unidirectionally; oligo-dt primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC Library."
BASE COUNT	256 a 254 c 236 g 271 t 2 others
ORIGIN	
Query Match	46.5%; Score 722; DB 12; Length 1019;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 722; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	187 AGTCCACAGACAGCTCGGCTTGTAGATCCCGATCTGCAATCTTCCGCTCTTCA
Db	49 AGTCCACAGACAGCTCGGCTTGTAGATCCCGATCTGCAATCTTCCGCTCTTCA
QY	247 GATTTGAAGGCT
Db	109 GATTTGAAGGCT
QY	307 TTGGGCAATGTTGGATTTACTGTTGGAACCAAGCCACACATCTGTAATCTCT
Db	169 TTGGGCAATGTTGGATTTACTGTTGGAACCAAGCCACACATCTGTAATCTCT
QY	367 CCGGACCAATGACCTGAGAGAGTGAAGTGAAGAGTGGTCTCAAAAGAGCAGACT
Db	229 CCGGACCAATGACCTGAGAGAGTGAAGTGAAGAGTGGTCTCAAAAGAGCAGACT
QY	427 CATTCCTCTACCATCCGCTATCTCTCGACCATGAAGCGCATTAACCTGGAACATG
Db	289 CATTCCTCTACCATCCGCTATCTCTCGACCATGAAGCGCATTAACCTGGAACATG
QY	487 GAAGAGCGCTGCTGATCCGGCTCTGGAAGAACAGTCCGATCTCTCTCTATAC
Db	349 GAAGAGCGCTGCTGATCCGGCTCTGGAAGAACAGTCCGATCTCTCTCTATAC
QY	547 AGCCTATGATGCTGCGCCCGAGGCGCTCAACACTGTTGGCTAAAGGCTTGGACTTG
Db	409 AGCCTATGATGCTGCGCCCGAGGCGCTCAACACTGTTGGCTAAAGGCTTGGACTTG
QY	607 TACCTCAGGCGCATCATCTCTTCAAAAGCTCCCACTACCTCAAGAGGAAACACCG
Db	469 TACCTCAGGCGCATCATCTCTTCAAAAGCTCCCACTACCTCAAGAGGAAACACCG
QY	667 AGTGAATTCACGTTAACTACACCCCAAGACCTGGCAAGATCTCTGCAAGTGAAG
Db	529 AGTGAATTCACGTTAACTACACCCCAAGACCTGGCAAGATCTCTGCAAGTGAAG
QY	727 AATTGAGGCTTCTGCTCACTCTTTCTGCTAGAGCTGTAATGAGAGAAACACAG
Db	589 AATTGAGGCTTCTGCTCACTCTTTCTGCTAGAGCTGTAATGAGAGAAACACAG


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/clone="IMAGE:334609"
/issue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone.lib="NIH_MGC_20"
/Note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      191 a      196 c      173 g      198 t
ORIGIN

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Query Match      43.6%; Score 677; DB 10; Length 759;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 TTGTAGATTCCCTGATCTGCATATCTTCCCGTTCCTTCATGATTTGAAGGCTCTCTTT 266
    |||||||
DB 48 TTGTAGATTCCCTGATCTGCATATCTTCCCGTTCCTTCATGATTTGAAGGCTCTCTTT 107
    |||||||

QY 267 CTTCCTGATGATCTTGCATCCCTCTCTGCTGAGAGTTGGACATGTTGATAC 326
    |||||||
DB 108 CTTCCTGATGATCTTGCATCCCTCTCTGCTGAGAGTTGGACATGTTGATAC 167
    |||||||

QY 327 TGGTGAACCAAGCCACACATACCTGTAATACCTCTCTGACCAATGACCTACCTG 386
    |||||||
DB 168 TGGTGAACCAAGCCACACATACCTGTAATACCTCTCTGACCAATGACCTACCTG 227
    |||||||

QY 387 AGGAAGTATGAGAGAGTGTCTGCAAAAGAGGACACCTATCTCTCTACCATCCG 446
    |||||||
DB 228 AGGAAGTATGAGAGAGTGTCTGCAAAAGAGGACACCTATCTCTCTACCATCCG 287
    |||||||

QY 447 CATCTCTCCGACCCAGGAGCGCATACCTGGAACACATGGAAGAGCGCTGCTATCC 506
    |||||||
DB 288 CATCTCTCCGACCCAGGAGCGCATACCTGGAACACATGGAAGAGCGCTGCTATCC 347
    |||||||

QY 507 GGGCTCTGAGAGACAGAGTCGGTATCTACTCTCTCATACAGCCTATGATGCTGCGCC 566
    |||||||
DB 348 GGGCTCTGAGAGACAGAGTCGGTATCTACTCTCTCATACAGCCTATGATGCTGCGCC 407
    |||||||

QY 567 AGGCGCTCAACAACCTGTTGGCTAAAGGCTTGGAGCTTGTACCTCAGGCCATACATC 626
    |||||||
DB 408 AGGCGCTCAACAACCTGTTGGCTAAAGGCTTGGAGCTTGTACCTCAGGCCATACATC 467
    |||||||

QY 627 CTTCCAAAGCTCCCACTACCTACAGAGAGGAACACGAGTATGATTAACGTTAACT 686
    |||||||
DB 468 CTTCCAAAGCTCCCACTACCTACAGAGAGGAACACGAGTATGATTAACGTTAACT 527
    |||||||

QY 687 ACAACCAAGACCTGACAAAGTCACTGCTGACGTGAAGAGAAATGACGGTCTTCTGCA 746
    |||||||
DB 528 ACAACCAAGACCTGACAAAGTCACTGCTGACGTGAAGAGAAATGACGGTCTTCTGCA 587
    |||||||

QY 747 CTTCCTTTTCTGCTAGAGCTGTAATGAGAGACAAACAGGATTAATCTGAATTTACTC 806
    |||||||
DB 588 CTTCCTTTTCTGCTAGAGCTGTAATGAGAGACAAACAGGATTAATCTGAATTTACTC 647
    |||||||

QY 807 AGAAGCTTTGATGACAGTGTGATGATTTCTTCCCGGAACAACAACCTTATCAGAGA 866
    |||||||
DB 648 AGAAGCTTTGATGACAGTGTGATGATTTCTTCCCGGAACAACAACCTTATCAGAGA 707
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QY 867 CGGAATTCGTGCTAGT 883
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DB 708 CGGAATTCGTGCTAGT 724
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RESULT 13
B0526538      919 bp      mRNA      linear      EST 13-SEP-2002
LOCUS        B0526538
DEFINITION   AGENCOURT_10181989 NIH_MGC_101 Homo sapiens cDNA clone
IMAGE:6536226 5', mRNA sequence.

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ACCESSION      B0526538
VERSION        B0526538.1
KEYWORDS      GI:22836979
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE         NIH-MGC http://img.nci.nih.gov/
JOURNAL       National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT       Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2697 row: d column: 18
High quality sequence stop: 696.
Location/Qualifiers
1. 919
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6536226"
/issue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone.lib="NIH_MGC_101"
/Note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2:
XhoI; cDNA made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

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BASE COUNT      230 a      226 c      229 g      228 t      6 others
ORIGIN
Query Match      43.5%; Score 675; DB 13; Length 919;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 675; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGATTTATCTTGGTGTGCTGACAGAGACAGCAAGAGAGATTTGGTCAGAAAATCG 60
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DB 24 GTGATTTATCTTGGTGTGCTGACAGAGACAGCAAGAGAGATTTGGTCAGAAAATCG 83
    |||||||

QY 61 CTTGCCGACACAGACAGCGCATGATGAGGACAGGGGCTCTGACTCAGACTTAACCTG 120
    |||||||
DB 84 CTTGCCGACACAGACAGCGCATGATGAGGACAGGGGCTCTGACTCAGACTTAACCTG 143
    |||||||

QY 121 CTGTGCTGCTGCTTTTCTCTCTGCTGCAAAAAGGCTGAAAGTGGCACTGAATGAGCA 180
    |||||||
DB 144 CTGTGCTGCTGCTTTTCTCTCTGCTGCAAAAAGGCTGAAAGTGGCACTGAATGAGCA 203
    |||||||

QY 181 TAGATGATCCGACGACAGTCCGGTTTGATGATCCGATGCAATCTCCCGCTG 240
    |||||||
DB 204 TAGATGATCCGACGACAGTCCGGTTTGATGATCCGATGCAATCTCCCGCTG 263
    |||||||

QY 241 CTTCATGATTTGAAGGCTCTCTCTCTCTCTGGAATGATTTGCAATCCCTCGTTTCG 300
    |||||||
DB 264 CTTCATGATTTGAAGGCTCTCTCTCTCTCTGGAATGATTTGCAATCCCTCGTTTCG 323
    |||||||

QY 301 TGAGAGTTGGGACAAATGTTGATTTACTGTGGAACCAAGCCACCAATCTGTAATAC 360
    |||||||
DB 324 TGAGAGTTGGGACAAATGTTGATTTACTGTGGAACCAAGCCACCAATCTGTAATAC 383
    |||||||

QY 361 ACTCTTCCTGACCAATGACTGACTGAGAGAGAGATGAGAGAGAGTCTGCAAAAAGAGC 420
    |||||||
DB 384 ACTCTTCCTGACCAATGACTGACTGAGAGAGAGATGAGAGAGAGTCTGCAAAAAGAGC 443
    |||||||

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QY 421 AGACCTATTCTCTCTACCAATCCGCTATCTTCGAGCCATGAAGCGCATACCTGGAA 480
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Db 444 AGACCTATTCTCTCTACCAATCCGCTATCTTCGAGCCATGAAGCGCATACCTGGAA 503
QY 481 CACATGGAAGAGGCGCTGTGTATCCGGCTCTGAGAACAGAGTGGTATCTACTCTCC 540
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Db 504 CACATGGAAGAGGCGCTGTGTATCCGGCTCTGAGAACAGAGTGGTATCTACTCTCC 563
QY 541 TCATACAGCTTATATGCTGCGCCCAAGGCGTCAACAATGTTGGCTAAAGGCGTTGG 600
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Db 564 TCATACAGCTTATATGCTGCGCCCAAGGCGTCAACAATGTTGGCTAAAGGCGTTGG 623
QY 601 AGCTTACCTCCAGGCGCATACATCTCTCCAAAGCTCCCAACTACCTACAGAGGAAA 660
|||||
Db 624 AGCTTACCTCCAGGCGCATACATCTCTCCAAAGCTCCCAACTACCTACAGAGGAAA 683
QY 661 CCACCGAGTAGAATT 675
|||||
Db 684 CCACCGAGTAGAATT 698

RESULT 14
BQ437698 877 bp mRNA linear EST 24-MAY-2002
LOCUS AGENCOURT.7894666 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6158334
DEFINITION 5', mRNA sequence.

ACCESSION BQ437698
VERSION BQ437698.1 GI:21176774
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 877)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCID/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LLM13505 row: k column: 07
High quality sequence stop: 667.
Location/Qualifiers

FEATURES
source

1. 877
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/mol_type="mRNA"
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/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
BASE COUNT 247 a 181 c 206 g 242 t 1 others
ORIGIN

Query Match 43.4%; Score 674; DB 13; Length 877;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 651 CAGAGGGAACACCGAGTAGAATTCAAGTTACTACACCAAGAGCTGACAAAGTCA 710
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Db 24 CAGAGGGAACACCGAGTAGAATTCAAGTTACTACACCAAGAGCTGACAAAGTCA 83

QY 711 TGCTCGAGTGAAGAAATGACGGTGTCTGTCTACATCTTTTCTCTAGAGCTGTA 770
|||||
Db 84 TGCTCGAGTGAAGAAATGACGGTGTCTGTCTACATCTTTTCTCTAGAGCTGTA 143
QY 771 ATGAGAAACAACACGGATTATCTGAATTTGTAATCTCAGAAAGCTTTGATGAGGTGTAG 830
|||||
Db 144 ATGAGAAACAACACGGATTATCTGAATTTGTAATTTACTCAGAAAGCTTTGATGAGGTGTAG 203
QY 831 ATTTTCTTTCCCGGACAAACATTTATCTCAGAAAGAGGAAATCTGTCACTGAGAAAGC 890
|||||
Db 204 ATTTTCTTTCCCGGACAAACATTTATCTCAGAAAGAGGAAATCTGTCACTGAGAAAGC 263
QY 891 CTGTGCTCTCATACTGTAATGAGAGGATATGACACTGATGAATCTGTCCCTGG 950
|||||
Db 264 CTGTGCTCTCATACTGTAATGAGAGGATATGACACTGATGAATCTGTCCCTGG 323
QY 951 CAACCATGATTGATCGAATAAAGACACCTAAACATATCTCATATTCCTTAGCCCTTG 1010
|||||
Db 324 CAACCATGATTGATCGAATAAAGACACCTAAACATATTCCTTAGCCCTTG 383
QY 1011 GGTGGGGAACACCTTAGAGTCTCAAGTCAAAAGTCGTGGCCCTGTCTGTGGGA 1070
|||||
Db 384 GGTGGGGAACACCTTAGAGTCTCAAGTCAAAAGTCGTGGCCCTGTCTGTGGGA 443
QY 1071 GCAGGCTCTCAGAGGCTGTAGGCTGACCTTACCTCAGAGTGAAGATGCCATCATG 1130
|||||
Db 444 GCAGGCTCTCAGAGGCTGTAGGCTGACCTTACCTCAGAGTGAAGATGCCATCATG 503
QY 1131 ATACTTTGGATGCTGCTTCCCAAGAAATTAATGTCATCCTGTGAAACACAGACACTG 1190
|||||
Db 504 ATACTTTGGATGCTGCTTCCCAAGAAATTAATGTCATCCTGTGAAACACAGACACTG 563
QY 1191 AACGAGGCTTCTTTCTTACCTTGAGATATGTCGATTCCTGACACTTGGAAATTAAGATTA 1250
|||||
Db 564 AACGAGGCTTCTTTCTTACCTTGAGATATGTCGATTCCTGACACTTGGAAATTAAGATTA 623
QY 1251 ATATTATCTTATCAGAGACTGACAGAGGACCTCTTACAGGTGATTAATTCGAAACATC 1310
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Db 624 ATATTATCTTATCAGAGACTGACAGAGGACCTCTTACAGGTGATTAATTCGAAACATC 683
QY 1311 AGATTAACACATTC 1324
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Db 684 AGATTAACACATTC 697

RESULT 15
BE797115 963 bp mRNA linear EST 20-SEP-2000
LOCUS 601587094F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941518 5',
DEFINITION mRNA sequence.

ACCESSION BE797115
VERSION BE797115.1 GI:10218313
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 963)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCID/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at: Image.llnl.gov
Plate: LLM793 row: k column: 23
High quality sequence stop: 756.
Location/Qualifiers

FEATURES
source

1. 963

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/lab_host="DH10B (phage-resistant)"  
/clone_lib="NIH_MGC_7"  
/note="Organ: lung; Vector: pOT87; Site_1: XhoI; Site_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(s). Size selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
BASE COUNT      239 a      254 c      226 g      244 t  
ORIGIN
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Query Match      42.0%; Score 652; DB 10; Length 963;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 652; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY      202 CCGGTTGTAGATTCCTGATCGCAATCTCCCGTCTCATGATGATTTGAAGCTCT 261  
      |||  
Db      1 CCGGTTGTAGATTCCTGATCGCAATCTCCCGTCTCATGATGATTTGAAGCTCT 60  
  
QY      262 CCTTCTTCCTTGAATGACTTTGATCCCTCTGTTGCTGAGAGTTGGACAATGTTG 321  
      |||  
Db      61 CCTTCTTCCTTGAATGACTTTGATCCCTCTGTTGCTGAGAGTTGGACAATGTTG 120  
  
QY      322 ATTACTGTGGAACCAAGCCACACATCTGTAATATACATCTTCCCTGACCAATGACT 381  
      |||  
Db      121 ATTACTGTGGAACCAAGCCACACATCTGTAATATACATCTTCCCTGACCAATGACT 180  
  
QY      382 GACTGAGGAATGATGAGAGAGTCTGCAAAAAGAGGACCTATTCTCTCTACCA 441  
      |||  
Db      181 GACTGAGGAATGATGAGAGAGTCTGCAAAAAGAGGACCTATTCTCTCTACCA 240  
  
QY      442 TCCGCTATCTTCGACCACTGAAGGCATTAACCTGGAACATGGAAGAGCGCCCTGT 501  
      |||  
Db      241 TCCGCTATCTTCGACCACTGAAGGCATTAACCTGGAACATGGAAGAGCGCCCTGT 300  
  
QY      502 GATCCGGGCTCTGGAACAAGTCTGATCTCTCTCATACAGCCTATGATGCTGC 561  
      |||  
Db      301 GATCCGGGCTCTGGAACAAGTCTGATCTCTCTCATACAGCCTATGATGCTGC 360  
  
QY      562 GCCCGAGGGGCTCAAACTGCTGCTAAAGGCTTGGAGCTTGACTCCAGGCCAT 621  
      |||  
Db      361 GCCCGAGGGGCTCAAACTGCTGCTAAAGGCTTGGAGCTTGACTCCAGGCCAT 420  
  
QY      622 ACATCCTTCCAAAGCTCCCAACTACCTACAGAGGAAACACCGAGTAGAATTCACGT 681  
      |||  
Db      421 ACATCCTTCCAAAGCTCCCAACTACCTACAGAGGAAACACCGAGTAGAATTCACGT 480  
  
QY      682 TAACTACACCAAGACCTGGAACAAGTCACTGTCAGTGAAGAATTGACGGTCTTC 741  
      |||  
Db      481 TAACTACACCAAGACCTGGAACAAGTCACTGTCAGTGAAGAATTGACGGTCTTC 540  
  
QY      742 TGTCACTTCTTTTCTGCTAGGACTGATATGAGAAACAACACGATTAATCTGAATTG 801  
      |||  
Db      541 TGTCACTTCTTTTCTGCTAGGACTGATATGAGAAACAACACGATTAATCTGAATTG 600  
  
QY      802 TACTCAGAGGCTTTGATCAGGTGTAGATTTTCTTCCCGGACAAACAA 853  
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Db      601 TACTCAGAGGCTTTGATCAGGTGTAGATTTTCTTCCCGGACAAACAA 652
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Job time : 2396 secs